

SEQUENCE LISTING

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AOKI, TOSHIO
AKASHI, TOMOYOSHI

<120> POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE SYNTHASE

<130> JKM-001

<140> 09/890,646

<141> 2001-08-02

<150> PCT/JP00/00596

<151> 2000-02-04

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1895

<212> DNA

<213> Glycyrrhiza echinata

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<221> CDS

<222> (144)..(1712)

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acttctctct atactcgact ctttgttatt agttatcatt attattatta caccattaaa 120

gtagcaaaga tcaaacaac acc atg ttg gtg gaa ctt gca att act ctg ttg 173

Met Leu Val Glu Leu Ala Ile Thr Leu Leu
1 5 10

gtg ata gcc ctg ttc ata cac ctg cgt ccc aca cta agt gca aaa tca 221

Val Ile Ala Leu Phe Ile His Leu Arg Pro Thr Leu Ser Ala Lys Ser
15 20 25

aag tcc ctt cgc cac ctc cca aac cct cca agt cca aaa ccc cgt ctc 269

Lys Ser Leu Arg His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu
30 35 40

cca ttt gtg ggt cac ctt cac ctt tta gac aaa ccc ctt ctc cac tac 317

Pro Phe Val Gly His Leu His Leu Leu Asp Lys Pro Leu Leu His Tyr
45 50 55

tcc ctc atc gac cta agc aaa cgc tat ggt ccg ctt tac tcc ctc tac 365

Ser Leu Ile Asp Leu Ser Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr
60 65 70

ttc ggt tcc atg cca acc gtt gta gcc tcc acc cct gaa ctt ttc aaa 413

Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys
75 80 85 90

ctc ttc ctc caa act cac gag gcc tct tcc ttc aac aca agg ttc caa	461
Leu Phe Leu Gln Thr His Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln	
95 100 105	
acc tct gcc att agg cgc cta acc tac gac aac tct gtt gcc atg gtt	509
Thr Ser Ala Ile Arg Arg Leu Thr Tyr Asp Asn Ser Val Ala Met Val	
110 115 120	
ccc ttt ggt cct tac tgg aag ttc att agg aag ctc atc atg aac gac	557
Pro Phe Gly Pro Tyr Trp Lys Phe Ile Arg Lys Leu Ile Met Asn Asp	
125 130 135	
ctc ctc aat gcc aca act gtg aac aag ttg agg cct tta agg agc caa	605
Leu Leu Asn Ala Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Ser Gln	
140 145 150	
gaa atc cga aag gtc ctc agg gtg atg gca cag agt gct gag tct cag	653
Glu Ile Arg Lys Val Leu Arg Val Met Ala Gln Ser Ala Glu Ser Gln	
155 160 165 170	
gtc cca ctt aat gtc acc gag gag ctt ctc aag tgg acc aac agc acc	701
Val Pro Leu Asn Val Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr	
175 180 185	
atc tcg agg atg atg ctt ggg gaa gca gag gaa atc agg gac ata gca	749
Ile Ser Arg Met Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala	
190 195 200	
cgt gac gtg ctt aag atc ttt ggg gag tat agt ctc acc gac ttc atc	797
Arg Asp Val Leu Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile	
205 210 215	
tgg ccc ttg aag aaa ctc aag gtt ggg caa tac gag aag agg att gac	845
Trp Pro Leu Lys Lys Leu Lys Val Gly Gln Tyr Glu Lys Arg Ile Asp	
220 225 230	
gat ata ttc aac agg ttt gac ccc gtc att gag agg gtc atc aag aaa	893
Asp Ile Phe Asn Arg Phe Asp Pro Val Ile Glu Arg Val Ile Lys Lys	
235 240 245 250	
aga cag gag att agg aag aag agg aag gag agg aat ggt gag atc gag	941
Arg Gln Glu Ile Arg Lys Lys Arg Lys Glu Arg Asn Gly Glu Ile Glu	
255 260 265	
gag ggt gaa cag agt gtg gtt ttt ctc gac act ttg ctc gat ttt gct	989
Glu Gly Glu Gln Ser Val Val Phe Leu Asp Thr Leu Leu Asp Phe Ala	
270 275 280	
gag gac gag acc atg gag atc aaa atc acc aag gaa caa atc aag ggc	1037
Glu Asp Glu Thr Met Glu Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly	
285 290 295	
ctt gtt gtg gat ttc ttc tca gca ggg acg gat tcc acg gcg gtg gca	1085
Leu Val Val Asp Phe Phe Ser Ala Gly Thr Asp Ser Thr Ala Val Ala	
300 305 310	

aca gac tgg gct ctg tca gag ctc atc aac aac ccc agg gtg ttt caa	1133
Thr Asp Trp Ala Leu Ser Glu Leu Ile Asn Asn Pro Arg Val Phe Gln	
315 320 325 330	
aag gca cga gag gag atc gat gcc gtc gtg gga aaa gac aga ctc gtt	1181
Lys Ala Arg Glu Glu Ile Asp Ala Val Val Gly Lys Asp Arg Leu Val	
335 340 345	
gac gag gca gat gtc cag aac ctt cct tac att aga tcc atc gtg aag	1229
Asp Glu Ala Asp Val Gln Asn Leu Pro Tyr Ile Arg Ser Ile Val Lys	
350 355 360	
gag acg ttc cgc atg cac cca cca cta ccc gtg gtc aaa aga aag tgc	1277
Glu Thr Phe Arg Met His Pro Pro Leu Pro Val Val Lys Arg Lys Cys	
365 370 375	
gtg cag gag tgt gag gtc gac ggt tat gtg atc cca gag gga gca ttg	1325
Val Gln Glu Cys Glu Val Asp Gly Tyr Val Ile Pro Glu Gly Ala Leu	
380 385 390	
atc ctt ttc aat gtt tgg gcc gtc gga aga gac cca aaa tac tgg gac	1373
Ile Leu Phe Asn Val Trp Ala Val Gly Arg Asp Pro Lys Tyr Trp Asp	
395 400 405 410	
agg ccc act gag ttc cgt ccc gaa agg ttc tta gaa aat gtg ggt gaa	1421
Arg Pro Thr Glu Phe Arg Pro Glu Arg Phe Leu Glu Asn Val Gly Glu	
415 420 425	
ggg gat caa gcc gtt gac ctt agg ggt caa cat ttc caa ctt ctt ccg	1469
Gly Asp Gln Ala Val Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro	
430 435 440	
ttt ggg tct gga agg agg atg tgc cct ggc gtc aat ttg gcc act gcg	1517
Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ala	
445 450 455	
gga atg gcc aca ctg ctt gcg tca gtt atc cag tgc ttt gat ctc agc	1565
Gly Met Ala Thr Leu Leu Ala Ser Val Ile Gln Cys Phe Asp Leu Ser	
460 465 470	
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Val Val Gly Pro Gln Gly Lys Ile Leu Lys Gly Asn Asp Ala Lys Val	
475 480 485 490	
agc atg gaa gag aga gct gga ctc acg gtt cca agg gca cat aac ctc	1661
Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala His Asn Leu	
495 500 505	
atc tgt gtc ccg gtt gca aga tca agt gcc gta ccc aaa ctc ttt tcg	1709
Ile Cys Val Pro Val Ala Arg Ser Ser Ala Val Pro Lys Leu Phe Ser	
510 515 520	
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Ser	
ataataattt tcaataaggt atcaatcaat gatatataga caatgatacc catatatcat	1822
cttcgcgact agtctctctt tggtacagta tggtgtaaca gcttaaatct atataatttt	1882

tactcgcata tcc

1895

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 <213> Glycyrrhiza echinata

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 His Leu Arg Pro Thr Leu Ser Ala Lys Ser Lys Ser Leu Arg His Leu
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 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Val Gly His Leu
 35 40 45
 His Leu Leu Asp Lys Pro Leu Leu His Tyr Ser Leu Ile Asp Leu Ser
 50 55 60
 Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr Phe Gly Ser Met Pro Thr
 65 70 75 80
 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
 85 90 95
 Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
 100 105 110
 Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 115 120 125
 Lys Phe Ile Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Lys Leu Arg Pro Leu Arg Ser Gln Glu Ile Arg Lys Val Leu
 145 150 155 160
 Arg Val Met Ala Gln Ser Ala Glu Ser Gln Val Pro Leu Asn Val Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Arg Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Asp Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys Lys Leu
 210 215 220
 Lys Val Gly Gln Tyr Glu Lys Arg Ile Asp Asp Ile Phe Asn Arg Phe
 225 230 235 240
 Asp Pro Val Ile Glu Arg Val Ile Lys Lys Arg Gln Glu Ile Arg Lys
 245 250 255

Lys Arg Lys Glu Arg Asn Gly Glu Ile Glu Glu Gly Glu Gln Ser Val
 260 265 270
 Val Phe Leu Asp Thr Leu Leu Asp Phe Ala Glu Asp Glu Thr Met Glu
 275 280 285
 Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe
 290 295 300
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Asp Trp Ala Leu Ser
 305 310 315 320
 Glu Leu Ile Asn Asn Pro Arg Val Phe Gln Lys Ala Arg Glu Glu Ile
 325 330 335
 Asp Ala Val Val Gly Lys Asp Arg Leu Val Asp Glu Ala Asp Val Gln
 340 345 350
 Asn Leu Pro Tyr Ile Arg Ser Ile Val Lys Glu Thr Phe Arg Met His
 355 360 365
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Val Gln Glu Cys Glu Val
 370 375 380
 Asp Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
 385 390 395 400
 Ala Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Thr Glu Phe Arg
 405 410 415
 Pro Glu Arg Phe Leu Glu Asn Val Gly Glu Gly Asp Gln Ala Val Asp
 420 425 430
 Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg
 435 440 445
 Met Cys Pro Gly Val Asn Leu Ala Thr Ala Gly Met Ala Thr Leu Leu
 450 455 460
 Ala Ser Val Ile Gln Cys Phe Asp Leu Ser Val Val Gly Pro Gln Gly
 465 470 475 480
 Lys Ile Leu Lys Gly Asn Asp Ala Lys Val Ser Met Glu Glu Arg Ala
 485 490 495
 Gly Leu Thr Val Pro Arg Ala His Asn Leu Ile Cys Val Pro Val Ala
 500 505 510
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<212> DNA

<213> Glycyrrhiza echinata

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 caaggttagc atggaagaga gagctggact cacggttcca agggcacata acctcatctg 180
 tgtcccgggt gcaagatcaa gtgccgtacc caaactcttt tcgtcgtaaa acatacgcgc 240
 gacaccacag aaagttgcca tggcatgatg cttttttatat aataattttc aataagggtat 300
 caatcaatga tatatagaca atgataccca tatatcatct tcacgactag tctctctttg 360
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<400> 5
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<210> 6
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 <212> PRT
 <213> Artificial Sequence

<220>
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 1 5 10

<210> 7
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<223> i

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23

<210> 9

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 9

aatacgactc actatag

17

<210> 10

<211> 17

<212> DNA

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<223> Description of Artificial Sequence: Primer

<400> 10

attaaccctc actaaag

17

<210> 11

<211> 27

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<223> Description of Artificial Sequence: Primer

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aaacaggatc catgttggtg gaacttg

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<210> 12

<211> 26

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<210> 13

<211> 27

<212> DNA

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<223> Description of Artificial Sequence: Primer

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27

<210> 14

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gaccggcaac aggattcaat cttaag

26